

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:41:26 / Search time 142 Seconds
(without alignments)
963.889 Million cell updates/sec

Title: US-10-604-944A-14

Perfect score: 77
Sequence: 1 ttaccctatagtcagacaa.....aactttaatgcatggytraa 77

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
6: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
7: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
8: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
9: /cgn2_6/ptodata/1/ina/6 COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	77	100.0	840	2	US-07-979-966A-1
2	77	100.0	845	2	US-08-589-446-3
3	77	100.0	845	2	US-08-444-882-3
4	77	100.0	845	2	US-08-389-459A-3
5	77	100.0	845	2	US-08-987-867A-3
6	77	100.0	1314	3	US-08-397-794A-1
7	77	100.0	2095	2	US-08-333-901-5
8	77	100.0	2095	2	US-08-456-582-5
9	77	100.0	2095	2	US-08-898-789-5
10	77	100.0	3807	2	US-08-417-210A-78
11	77	100.0	3807	2	US-09-136-159A-78
12	77	100.0	4307	3	US-09-552-950-1
13	77	100.0	4307	3	US-09-936-572-1
14	77	100.0	4338	3	US-09-872-733A-1
15	77	100.0	5362	3	US-08-463-209-5
16	77	100.0	5362	3	US-08-463-209-5
17	77	100.0	5362	3	US-08-463-209-5
18	77	100.0	7228	2	US-08-850-049-128
19	77	100.0	7228	2	US-08-850-049-128
20	77	100.0	7228	2	US-08-050-478-128
21	77	100.0	7228	2	US-08-050-478-128
22	77	100.0	7228	2	US-09-414-117-128
23	77	100.0	7228	3	US-09-414-117-128
24	77	100.0	7228	3	US-09-678-437-128

25	77	100.0	7228	3	US-09-678-437-128	Sequence 129, App
26	77	100.0	7228	3	US-09-943-722-128	Sequence 128, App
27	77	100.0	7228	3	US-09-943-722-128	Sequence 129, App
28	77	100.0	8366	3	US-09-872-733A-6	Sequence 6, Appl1
29	77	100.0	8560	3	US-09-936-572-11	Sequence 11, Appl1
30	77	100.0	8932	3	US-09-124-900-1	Sequence 4, Appl1
31	77	100.0	8933	3	US-08-463-210-4	Sequence 3, Appl1
32	77	100.0	8933	3	US-09-620-958A-3	Sequence 4, Appl1
33	77	100.0	8933	3	US-09-620-958A-4	Sequence 3, Appl1
34	77	100.0	8933	3	US-09-620-958A-9	Sequence 9, Appl1
35	77	100.0	8933	3	US-08-463-028-4	Sequence 9, Appl1
36	77	100.0	8933	3	US-08-463-209-4	Sequence 4, Appl1
37	77	100.0	8933	3	US-09-943-286-3	Sequence 3, Appl1
38	77	100.0	8933	3	US-09-943-286-4	Sequence 4, Appl1
39	77	100.0	8933	3	US-09-943-286-9	Sequence 9, Appl1
40	77	100.0	9609	3	US-09-827-688-4	Sequence 4, Appl1
41	77	100.0	9719	3	US-09-700-304-1	Sequence 1, Appl1
42	75.4	97.9	1503	3	US-09-393-795-2	Sequence 2, Appl1
43	75.4	97.9	7399	2	US-08-418-848A-9	Sequence 9, Appl1
44	75.4	97.9	9709	2	US-08-188-583-5	Sequence 5, Appl1
45	75.4	97.9	9709	3	US-08-388-353-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-07-979-966A-1
Sequence 1, Application US/07979966A
Patent No. 5707864
GENERAL INFORMATION:
APPLICANT: Myron E. Essex
APPLICANT: Xiaofang Yu
TITLE OF INVENTION: AIDS THERAPEUTICS BASED ON HIV
TITLE OF INVENTION: NA PEPTIDES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/979,966A
FILING DATE: No. 5707864member 23, 1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00379/018001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-979-966A-1
Query Match 100.0%; Score 77; DB 2; Length 840;

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:38:36 ; Search time 483 Seconds
(without alignments)
1062.487 Million cell updates/sec

Title: US-10-604-944A-14
Perfect score: 77
Sequence: 1 ttaccctatagtcagagaca.....aacttaaatcatgag99taaa 77

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001a:*
- 5: geneseqn2001b:*
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- 7: geneseqn2002b:*
- 8: geneseqn2003a:*
- 9: geneseqn2003b:*
- 10: geneseqn2003c:*
- 11: geneseqn2003d:*
- 12: geneseqn2004a:*
- 13: geneseqn2004b:*
- 14: geneseqn2005a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	566	1	AAAN71252
2	77	100.0	630	6	ABK14492
3	77	100.0	729	1	AAAN91288
4	77	100.0	801	1	AAAN91141
5	77	100.0	840	2	AAQ66839
6	77	100.0	845	2	AAQ680573
7	77	100.0	845	2	AAQ680573
8	77	100.0	876	1	AAAN60485
9	77	100.0	1092	10	ADBB87763
10	77	100.0	1092	10	ADBB87763
11	77	100.0	1092	10	ADBB87763
12	77	100.0	1092	10	ADBB87763
13	77	100.0	1179	10	ADBB87764
14	77	100.0	1179	10	ADBB87764
15	77	100.0	1179	10	ADBB87764
16	77	100.0	1179	10	ADBB87764
17	77	100.0	1179	10	ADBB87764
18	77	100.0	1308	10	ADBB87765
19	77	100.0	1308	10	ADBB87765

20	77	100.0	1308	12	AD105560	AD105560 Novel rec
21	77	100.0	1308	13	ADSB82122	ADSB82122 DNA seque
22	77	100.0	1317	2	AAQ90231	AAQ90231 HIV-1 gag
23	77	100.0	1320	1	AAAN90351	AAAN90351 Sequence
24	77	100.0	1424	1	AAAN80484	AAAN80484 Seq/Bg111
25	77	100.0	1496	10	ADBB87746	ADBB87746 HIV-1 gag
26	77	100.0	1496	10	ADBB87746	ADBB87746 HIV-1 gag
27	77	100.0	1496	10	ADBB87746	ADBB87746 HIV-1 gag
28	77	100.0	1496	10	ADBB87746	ADBB87746 HIV-1 gag
29	77	100.0	1503	1	ADBB82103	ADBB82103 Novel rec
30	77	100.0	1503	1	ADBB82103	ADBB82103 Novel rec
31	77	100.0	1503	6	ABV78254	ABV78254 HIV gag D
32	77	100.0	1503	6	ABX10073	ABX10073 HIV gag P
33	77	100.0	1503	6	ABX10073	ABX10073 HIV gag P
34	77	100.0	1503	8	ADBB81006	ADBB81006 HIV polyom
35	77	100.0	1503	9	ADBB81006	ADBB81006 HIV polyom
36	77	100.0	1503	11	ADBB81006	ADBB81006 HIV polyom
37	77	100.0	1503	12	ADBB81006	ADBB81006 HIV polyom
38	77	100.0	1503	13	ADBB81006	ADBB81006 HIV polyom
39	77	100.0	1512	1	AAAN92575	AAAN92575 Sequence
40	77	100.0	1515	10	ADBB81006	ADBB81006 HIV polyom
41	77	100.0	1515	10	ADBB81006	ADBB81006 HIV polyom
42	77	100.0	1515	10	ADBB81006	ADBB81006 HIV polyom
43	77	100.0	1515	10	ADBB81006	ADBB81006 HIV polyom
44	77	100.0	1515	10	ADBB81006	ADBB81006 HIV polyom
45	77	100.0	1560	1	AAAN90350	AAAN90350 Sequence

ALIGNMENTS

RESULT 1
ID AAAN71252 standard; DNA; 566 BP.
AC AAAN71252;
AC AAAN71252;
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 29-MAY-1991 (first entry)
DE Sequence of HTLV-III provirus nucleotides 653-1218, BMS-GAG, clone Gag-1.
DE HIV; AIDS; ARC; vaccine; diagnosis; immunoassay; ss.
KW Human T-lymphotropic virus III.
XX MO8704728-A.
XX PD 13-AUG-1987.
XX PF 03-FEB-1987; 87WO-US000225.
XX PR 03-FEB-1986; 86US-00825597.
XX PR 25-SEP-1986; 86US-00911455.
XX (CAME-) CAMBRIDGE BIOSCIENCE CORP.
XX Beltz G, Thorn RM, Marciani DJ, Hung C, Beltz GA, Thorn RM;
XX Marciani DJ, Hung CH;
XX MPI, 1987-235361/33.
XX Peptide fragments immunoreactive with HTLV-III antibodies - obtd. by
XX expressing cloned fragmented HTLV-III provirus nucleotide sequences.
XX Disclosure; Fig 15; 85pp; English.
XX The patent claims a peptide fragment which is immunoreactive to
XX antibodies against the HTLV-III virus and encoded for by the HTLV-III
XX provirus nucleotide sequences selected from nucleotides 653 to 1218, 2600
XX to 3911, 2743 to 4211, 6619 to 7198, and 7199 to 8052. The peptide
XX fragments are specifically recognised by antibodies produced in response

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:52:42 / Search time 405 Seconds
(without alignments)
157.929 Million cell updates/sec

Title: US-10-604-944A-14

Perfect score: 77
Sequence: 1 ttaccctatgctgagacac.....aacttaaatcgtggttaa 77

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 6059551 seqs, 41533918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA New:
1: /cgn2_6/ptodara/2/pubpna/US06_NEW_PUB.seq:
2: /cgn2_6/ptodara/2/pubpna/US06_NEW_PUB.seq:
3: /cgn2_6/ptodara/2/pubpna/US07_NEW_PUB.seq:
4: /cgn2_6/ptodara/2/pubpna/PCT_NEW_PUB.seq:
5: /cgn2_6/ptodara/2/pubpna/US09_NEW_PUB.seq:
6: /cgn2_6/ptodara/2/pubpna/US10_NEW_PUB.seq:
7: /cgn2_6/ptodara/2/pubpna/US10_NEW_PUB.seq:
8: /cgn2_6/ptodara/2/pubpna/US11_NEW_PUB.seq:
9: /cgn2_6/ptodara/2/pubpna/US11_NEW_PUB.seq:
10: /cgn2_6/ptodara/2/pubpna/US11_NEW_PUB.seq:
11: /cgn2_6/ptodara/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	1515	US-10-507-928-5	Sequence 5, Appli
2	77	100.0	1515	US-11-029-465-5	Sequence 5, Appli
3	77	100.0	9719	US-11-042-988-10	Sequence 10, Appli
4	75.4	97.9	1503	US-10-519-531-2	Sequence 2, Appli
5	75.4	97.9	15360	US-10-519-531-1	Sequence 1, Appli
6	75.4	97.9	17207	US-10-519-531-8	Sequence 8, Appli
7	45.6	59.2	1521	US-11-129-442-22	Sequence 22, Appli
8	44	57.1	1503	US-10-507-928-7	Sequence 3, Appli
9	44	57.1	1503	US-11-029-465-3	Sequence 7, Appli
10	44	57.1	1518	US-10-507-928-7	Sequence 7, Appli
11	44	57.1	1518	US-11-029-465-7	Sequence 7, Appli
12	42.4	55.1	1092	US-11-014-842A-40	Sequence 40, Appli
13	42.4	55.1	5278	US-11-124-602-2	Sequence 2, Appli
14	42.4	55.1	5304	US-11-124-602-1	Sequence 1, Appli
15	28.2	36.6	1329	US-10-750-185-37952	Sequence 1, Appli
16	28.2	36.6	1329	US-10-750-623-37952	Sequence 37952, A
17	26.4	34.3	1691140	US-11-091-018-1	Sequence 1, Appli
18	25.8	33.5	697	US-10-750-185-28849	Sequence 28849, A
19	25.8	33.5	697	US-10-750-623-28849	Sequence 28849, A
20	24.8	32.2	127340	US-11-112-908-36	Sequence 36, Appli
21	24.8	32.2	127340	US-11-112-908-35	Sequence 35, Appli
22	24.4	31.7	1086	US-10-750-185-32559	Sequence 32559, A

23	24.4	31.7	1086	US-10-750-623-32559	Sequence 32559, A
24	24.2	31.4	28033	US-10-829-826B-42	Sequence 42, Appli
25	24.2	31.4	28033	US-10-829-826B-43	Sequence 43, Appli
26	23.8	30.9	643	US-11-043-752-1480	Sequence 1480, Ap
27	23.8	30.9	1280	US-10-750-185-53636	Sequence 53636, A
28	23.8	30.9	1280	US-10-750-623-53636	Sequence 53636, A
29	23.8	30.9	387780	US-11-095-561-13259	Sequence 13259, A
30	23.6	30.6	480	US-10-219-146-33	Sequence 33, Appli
31	23.6	30.6	480	US-11-219-146-37	Sequence 37, Appli
32	23.6	30.6	480	US-11-219-146-37	Sequence 37, Appli
33	23.6	30.6	480	US-11-219-146-39	Sequence 39, Appli
34	23.6	30.6	600	US-11-219-146-43	Sequence 43, Appli
35	23.6	30.6	600	US-11-219-146-43	Sequence 43, Appli
36	23.6	30.6	600	US-11-219-146-45	Sequence 45, Appli
37	23.6	30.6	600	US-11-219-146-47	Sequence 47, Appli
38	23.6	30.6	752	US-11-219-146-17	Sequence 17, Appli
39	23.6	30.6	752	US-11-219-146-19	Sequence 19, Appli
40	23.6	30.6	752	US-11-219-146-21	Sequence 21, Appli
41	23.6	30.6	752	US-11-219-146-23	Sequence 23, Appli
42	23.6	30.6	1151	US-11-219-146-1	Sequence 1, Appli
43	23.6	30.6	1151	US-11-219-146-3	Sequence 3, Appli
44	23.6	30.6	1151	US-11-219-146-5	Sequence 5, Appli
45	23.6	30.6	1151	US-11-219-146-7	Sequence 7, Appli

ALIGNMENTS

EDJ

```

RESULT 1
US-10-507-928-5
: Sequence 5, Application US/10507928
: Publication No. US20050266024A1
: GENERAL INFORMATION:
: APPLICANT: POWDERED LIMITED AND GLAXO GROUP LIMITED
: TITLE OF INVENTION: ADJUVANT
: FILE REFERENCE: N. 88232B GCM
: CURRENT APPLICATION NUMBER: US/10/507,928
: CURRENT FILING DATE: 2004-09-17
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 5
: LENGTH: 1515
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: nucleotide sequence of the p17/24trNEF insert in p17/24trNEFI
US-10-507-928-5

Query Match          100.0%; Score 77; DB 7; Length 1515;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACCTATGTCGAGAACATCCAGGGGCAATGATCATCAGGCGCATATCAGCTAGAAC 60
Db 393 TTACCTATGTCGAGAACATCCAGGGGCAATGATCATCAGGCGCATATCAGCTAGAAC 452
QY 61 TTTAATGATGGGTAA 77
Db 453 TTTAATGATGGGTAA 469

RESULT 2
US-11-029-465-5
: Sequence 5, Application US/11029465
: Publication No. US20050256070A1
: GENERAL INFORMATION:
: APPLICANT: Braum, Ralph P.
: APPLICANT: Thomsen, Lindy
: APPLICANT: Van-Wely, Catherine
: APPLICANT: Ertel, Peter
: TITLE OF INVENTION: Adjuvant
: FILE REFERENCE: 033267-015
: CURRENT APPLICATION NUMBER: US/11/029,465

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:39:26 ; Search time 2175 Seconds
(without alignments)
2012.389 Million cell updates/sec

Title: US-10-604-944a-14

Perfect score: 77
Sequence: 1 ttaccctatgtagcagaca.....aactttaatgcatggtgta 77

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_in:*

3: gb_env:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pr:*

9: gb_ro:*

10: gb_sts:*

11: gb_sy:*

12: gb_un:*

13: gb_vi:*

14: gb_htg:*

15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	77	100.0	303 13 HIVM3S1	L21498 Human immu
2	77	100.0	303 13 HIVM4S1	L21499 Human immu
3	77	100.0	303 13 HIVM5S1	L21504 Human immu
4	77	100.0	303 13 HIVM6S1	L21508 Human immu
5	77	100.0	303 13 HIVM9S1	L21518 Human immu
6	77	100.0	330 13 ABI54280	ABI54280 Human imm
7	77	100.0	330 13 ABI54285	ABI54285 Human imm
8	77	100.0	330 13 ABI54295	ABI54295 Human imm
9	77	100.0	330 13 AY103237	AY103237 HIV-1 c10
10	77	100.0	426 13 AY103239	AY103239 HIV-1 c10
11	77	100.0	426 13 AY103240	AY103240 HIV-1 c10
12	77	100.0	426 13 AY103241	AY103241 HIV-1 c10
13	77	100.0	426 13 AY103242	AY103242 HIV-1 c10
14	77	100.0	426 13 AY103243	AY103243 HIV-1 c10
15	77	100.0	451 13 AF017925	AF017925 HIV-1 pat
16	77	100.0	502 13 AF116068	AF116068 HIV-1 iso
17	77	100.0	517 13 AF116050	AF116050 HIV-1 iso
18	77	100.0	536 13 AB112053	AB112053 Human imm

19	77	100.0	566 6 I01331	I01331 Sequence 1
20	77	100.0	566 6 I05038	I05038 Sequence 6
21	77	100.0	574 13 AB112051	AB112051 Human imm
22	77	100.0	574 13 AB112052	AB112052 Human imm
23	77	100.0	574 13 AB112056	AB112056 Human imm
24	77	100.0	574 13 AB112059	AB112059 Human imm
25	77	100.0	692 13 AY360925	AY360925 HIV-1 iso
26	77	100.0	729 6 A06256	A06256 pX1460 gag
27	77	100.0	735 13 AF071303	AF071303 HIV-1 iso
28	77	100.0	738 13 AF170634	AF170634 HIV-1 c10
29	77	100.0	840 6 I79824	I79824 Sequence 1
30	77	100.0	845 6 AR044674	AR044674 Sequence 1
31	77	100.0	845 6 I38635	I38635 Sequence 3
32	77	100.0	845 6 I40606	I40606 Sequence 3
33	77	100.0	876 6 A02736	A02736 Artificial
34	77	100.0	1089 13 AY656080	AY656080 HIV-1 iso
35	77	100.0	1093 13 AY134961	AY134961 HIV-1 iso
36	77	100.0	1093 13 AY134965	AY134965 HIV-1 iso
37	77	100.0	1094 13 AY134966	AY134966 HIV-1 iso
38	77	100.0	1095 13 AY134957	AY134957 HIV-1 iso
39	77	100.0	1095 13 AY134959	AY134959 HIV-1 iso
40	77	100.0	1095 13 AY134967	AY134967 HIV-1 iso
41	77	100.0	1308 6 E01254	E01254 DNA encodin
42	77	100.0	1424 6 A02742	A02742 Artificial
43	77	100.0	1424 6 A19610	A19610 Artificial
44	77	100.0	1455 6 A75892	A75892 Sequence 3
45	77	100.0	1464 6 A75896	A75896 Sequence 7

ALIGNMENTS

CDJ

RESULT 1
LOCUS HIVM3S1
DEFINITION Human immunodeficiency virus type 1, myristylated gag protein p17 (gag) gene, partial cds.
ACCESSION L21498.1
VERSION GI:424696
KEYWORDS gag gene; myristylated gag protein p17.
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
VIRUSES; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE 1 (Bases 1 to 303)
Zhu, T., Mo, H., Wang, N., Nam, D.S., Cao, Y., Koup, R.A. and Ho, D.D. Genotypic and phenotypic characterization of HIV-1 patients with primary infection
JOURNAL Science 261 (5125), 1179-1181 (1993)
PUBMED 8356453
COMMENT Original source text: Human immunodeficiency virus type 1 RNA.
FEATURES
source location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 77; DB 13; Length 303;
Best Local Similarity 100.0%; Pred. No. 8.2e-16;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTACCTATGTCAGAAATCCAGGGGCAATGTACATCAGCCATATCACTAGAAC 60